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RAW SEQUENCE LISTING

DATE: 04/26/2002

PATENT APPLICATION: US/10/067,457

TIME: 14:27:58

Input Set : N:\Crif3\RULE60\10067457.raw

Output Set: N:\CRF3\04262002\J067457.raw

1 <110> APPLICANT: Aventis Pharma Deutschland GmbH
2 <120> TITLE OF INVENTION: Process for identifying substances which modulate the
3 activity of hyperpolarization-activated cation channels
4 <130> FILE REFERENCE: AVE D-2000/A006
5 <140> CURRENT APPLICATION NUMBER: 10/067,457
6 <141> CURRENT FILING DATE: 2002-04-09
8 <150> PRIOR APPLICATION NUMBER: US/09/779,587
9 <151> PRIOR FILING DATE: 2001-02-09
13 <160> NUMBER OF SEQ ID NOS: 10
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 889
18 <212> TYPE: PRT
19 <213> ORGANISM: Homo sapiens
20 <400> SEQUENCE: 1
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22 1 5 10 15
23 Ser Pro Thr Thr Gly Pro Pro Pro Pro Pro Pro Pro Arg Pro Pro Lys
24 20 25 30
25 Gln Gln Pro Pro Pro Pro Pro Pro Ala Pro Pro Pro Gly Pro Gly
26 35 40 45
27 Pro Ala Pro Pro Gln His Pro Pro Arg Ala Glu Ala Leu Pro Pro Glu
28 50 55 60
29 Ala Ala Asp Glu Gly Gly Pro Arg Gly Arg Leu Arg Ser Arg Asp Ser
30 65 70 75 80
31 Ser Cys Gly Arg Pro Gly Thr Pro Gly Ala Ala Ser Thr Ala Lys Gly
32 85 90 95
33 Ser Pro Asn Gly Glu Cys Gly Arg Gly Glu Pro Gln Cys Ser Pro Ala
34 100 105 110
35 Gly Pro Glu Gly Pro Ala Arg Gly Pro Lys Val Ser Phe Ser Cys Arg
36 115 120 125
37 Gly Ala Ala Ser Gly Pro Ala Pro Gly Pro Gly Pro Ala Glu Glu Ala
38 130 135 140
39 Gly Ser Glu Glu Ala Gly Pro Ala Gly Glu Pro Arg Gly Ser Gln Ala
40 145 150 155 160
41 Ser Phe Met Gln Arg Gln Phe Gly Ala Leu Leu Gln Pro Gly Val Asn
42 165 170 175
43 Lys Phe Ser Leu Arg Met Phe Gly Ser Gln Lys Ala Val Glu Arg Glu
44 180 185 190
45 Gln Glu Arg Val Lys Ser Ala Gly Ala Trp Ile Ile His Pro Tyr Ser
46 195 200 205
47 Asp Phe Arg Phe Tyr Trp Asp Phe Thr Met Leu Leu Phe Met Val Gly
48 210 215 220

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49  Asn Leu Ile Ile Ile Pro Val Gly Ile Thr Phe Phe Lys Asp Glu Thr
50  225                230                235                240
51  Thr Ala Pro Trp Ile Val Phe Asn Val Val Ser Asp Thr Phe Phe Leu
52                245                250                255
53  Met Asp Leu Val Leu Asn Phe Arg Thr Gly Ile Val Ile Glu Asp Asn
54                260                265                270
55  Thr Glu Ile Ile Leu Asp Pro Glu Lys Ile Lys Lys Lys Tyr Leu Arg
56                275                280                285
57  Thr Trp Phe Val Val Asp Phe Val Ser Ser Ile Pro Val Asp Tyr Ile
58                290                295                300
59  Phe Leu Ile Val Glu Lys Gly Ile Asp Ser Glu Val Tyr Lys Thr Ala
60  305                310                315                320
61  Arg Ala Leu Arg Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg
62                325                330                335
63  Leu Leu Arg Leu Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu
64                340                345                350
65  Ile Phe His Met Thr Tyr Asp Leu Ala Ser Ala Val Met Arg Ile Cys
66                355                360                365
67  Asn Leu Ile Ser Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu
68                370                375                380
69  Gln Phe Leu Val Pro Met Leu Gln Asp Phe Pro Arg Asn Cys Trp Val
70  385                390                395                400
71  Ser Ile Asn Gly Met Val Asn His Ser Trp Ser Glu Leu Tyr Ser Phe
72                405                410                415
73  Ala Leu Phe Lys Ala Met Ser His Met Leu Cys Ile Gly Tyr Gly Arg
74                420                425                430
75  Gln Ala Pro Glu Ser Met Thr Asp Ile Trp Leu Thr Met Leu Ser Met
76                435                440                445
77  Ile Val Gly Ala Thr Cys Tyr Ala Met Phe Ile Gly His Ala Thr Ala
78                450                455                460
79  Leu Ile Gln Ser Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu Lys Tyr
80  465                470                475                480
81  Lys Gln Val Glu Gln Tyr Met Ser Phe His Lys Leu Pro Ala Asp Phe
82                485                490                495
83  Arg Gln Lys Ile His Asp Tyr Tyr Glu His Arg Tyr Gln Gly Lys Met
84                500                505                510
85  Phe Asp Glu Asp Ser Ile Leu Gly Glu Leu Asn Gly Pro Leu Arg Glu
86                515                520                525
87  Glu Ile Val Asn Phe Asn Cys Arg Lys Leu Val Ala Ser Met Pro Leu
88                530                535                540
89  Phe Ala Asn Ala Asp Pro Asn Phe Val Thr Ala Met Leu Thr Lys Leu
90  545                550                555                560
91  Lys Phe Glu Val Phe Gln Pro Gly Asp Tyr Ile Ile Arg Glu Gly Thr
92                565                570                575
93  Ile Gly Lys Lys Met Tyr Phe Ile Gln His Gly Val Val Ser Val Leu
94                580                585                590
95  Thr Lys Gly Asn Lys Glu Met Lys Leu Ser Asp Gly Ser Tyr Phe Gly
96                595                600                605
97  Glu Ile Cys Leu Leu Thr Arg Gly Arg Arg Thr Ala Ser Val Arg Ala

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98          610          615          620
99  Asp Thr Tyr Cys Arg Leu Tyr Ser Leu Ser Val Asp Asn Phe Asn Glu
100      625          630          635          640
101  Val Leu Glu Glu Tyr Pro Met Met Arg Arg Ala Phe Glu Thr Val Ala
102          645          650          655
103  Ile Asp Arg Leu Asp Arg Ile Gly Lys Lys Asn Ser Ile Leu Leu His
104          660          665          670
105  Lys Val Gln His Asp Leu Asn Ser Gly Val Phe Asn Asn Gln Glu Asn
106          675          680          685
107  Ala Ile Ile Gln Glu Ile Val Lys Tyr Asp Arg Glu Met Val Gln Gln
108      690          695          700
109  Ala Glu Leu Gly Gln Arg Val Gly Leu Phe Pro Pro Pro Pro Pro
110      705          710          715          720
111  Pro Gln Val Thr Ser Ala Ile Ala Thr Leu Gln Gln Ala Ala Ala Met
112          725          730          735
113  Ser Phe Cys Pro Gln Val Ala Arg Pro Leu Val Gly Pro Leu Ala Leu
114          740          745          750
115  Gly Ser Pro Arg Leu Val Arg Arg Pro Pro Pro Gly Pro Ala Pro Ala
116          755          760          765
117  Ala Ala Ser Pro Gly Pro Pro Pro Pro Ala Ser Pro Pro Gly Ala Pro
118          770          775          780
119  Ala Ser Pro Arg Ala Pro Arg Thr Ser Pro Tyr Gly Gly Leu Pro Ala
120      785          790          795          800
121  Ala Pro Leu Ala Gly Pro Ala Leu Pro Ala Arg Arg Leu Ser Arg Ala
122          805          810          815
123  Ser Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro His Gly Ala Pro
124          820          825          830
125  Gly Pro Ala Ala Ser Thr Arg Pro Ala Ser Ser Ser Thr Pro Arg Leu
126          835          840          845
127  Gly Pro Thr Pro Ala Ala Arg Ala Ala Ala Pro Ser Pro Asp Arg Arg
128          850          855          860
129  Asp Ser Ala Ser Pro Gly Ala Ala Gly Gly Leu Asp Pro Gln Asp Ser
130      865          870          875          880
131  Ala Arg Ser Arg Leu Ser Ser Asn Leu
132          885

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134 <210> SEQ ID NO: 2

135 <211> LENGTH: 3372

136 <212> TYPE: DNA

137 <213> ORGANISM: Homo sapiens

138 <400> SEQUENCE: 2

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139  cggctccgct ccgcactgcc cggcgccgcc tcgccatgga cgcgcgcggg ggcggcgggc 60
140  ggcccgggga gagcccgggc gcgagcccca cgaccgggcc gccgcgcgcg ccgccccgcg 120
141  gcccccccaa acagcagccg ccgcgcgcgc cgccgcccgc gcccccccg ggcggcgggc 180
142  ccgcgcccc ccagcaccgc ccccgggccg aggcgttgcc cccggaggcg gcggatgagg 240
143  gcggcccgcg gggccggctc cgcagccgcg acagctcgtg cggccgcccc ggcaccccg 300
144  gcgcggcgag cacggccaag ggcagcccg acggcgagtg cgggcgcggc gagccgcagt 360
145  gcagccccgc ggggcccag gggcgccgc gggggcccaa ggtgtcgttc tcgtgccgcg 420
146  gggcgccctc ggggcccgc ccggggccgc ggccggcgga ggaggcgggc agcaggagg 480
147  cgggcccggc gggggagccg cgcggcagcc aggcagctt catgcagcg cagttcggcg 540

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148   cgctcctgca gccgggcgct aacaagttct cgctgcggat gttcggcagc cagaaggccg 600
149   tggagcgcgga gcaggagcgc gtcaagtcgg cgggggcctg gatcatccac ccgtacagcg 660
150   acttcagggtt ctactgggac ttcacatgc tgctgttcat ggtgggaaac ctcacatca 720
151   tcccagtggtg catcaccttc ttcaaggatg agaccactgc cccgtggatc gtgttcaacg 780
152   tgggtctcgga caccttcttc ctcatggacc tgggtgtgaa cttccgcacc ggcattgtga 840
153   tcgaggacaa cacggagatc atcctggacc ccgagaagat caagaagaag tatctgcgca 900
154   cgtggttcgt ggtggacttc gtgtcctcca tccccgtgga ctacatcttc cttatcgtgg 960
155   agaagggcat tgactccgag gtctacaaga cggcacgcgc cctgcgcata gtgcgcttca 1020
156   ccaagatcct cagcctcctg cggctgctgc gcctctcacg cctgatccgc tacatccatc 1080
157   agtgggagga gatcttcac atgacctatg acctggccag cgcggtgatg aggatctgca 1140
158   atctcatcag catgatgctg ctgctctgcc actgggacgg ctgcctgcag ttcctggtgc 1200
159   ctatgctgca ggacttcccg cgcaactgct ggggtgtccat caatggcatg gtgaaccact 1260
160   cgtggagtga actgtactcc ttgcactct tcaaggccat gagccacatg ctgtgcacatg 1320
161   ggtacggcgg gcaggcgccc gagagcatga cggacatctg gctgaccatg ctcagcatga 1380
162   ttgtgggtgc cacctgctac gccatgttca tcggccacgc cactgccctc atccagtcgc 1440
163   tggactctc gcggcgccag taccaggaga agtacaagca ggtggagcag tacatgtcct 1500
164   tccacaagct gccagctgac ttccgccaga agatccacga ctactatgag caccgttacc 1560
165   agggcaagat gtttgacgag gacagcatcc tgggcgagct caacgggccc ctgcgggagg 1620
166   agatcgtcaa cttcaactgc cgggaagctg tggcctccat gccgctgttc gccaacgcgg 1680
167   accccaactt cgtcacggcc atgctgacca agctcaagtt cgaggtcttc cagcggggtg 1740
168   actacatcat ccgcgaaggc accatcgga agaagatgta cttcatccag cacggcggtg 1800
169   tcagcgtgct cactaagggc aacaaggaga tgaagctgtc cgatggctcc tacttcgggg 1860
170   agatctgctt gctcaccggg ggccgcccga cggcgagcgt gcgggctgac acctactgcc 1920
171   gcctctatct gctgagcgtg gacaacttca acgaggtgct ggaggagtac cccatgatgc 1980
172   ggcgcgccct cgagacggtg gccatcgacc gcctggaccg catcggaag aagaattcca 2040
173   tcctcctgca caagtgacg catgacctca actcgggcgt attcaacaac caggagaacg 2100
174   ccatcatcca ggagatcgtc aagtacgacc gcgagatggt gcagcaggcc gagctgggtc 2160
175   agcgcgtggg cctcttcccg ccgcccgcgc cgcgcgcgca ggtcacctcg gccatcgcca 2220
176   cgctgcagca ggcggcggcc atgagcttct gccgcgaggt ggcgcgcccg ctcggtggggc 2280
177   cgctggcgct cggtctcgcc cgctcgtgc gccgcgcgc ccggggggcc gcacctgccg 2340
178   ccgcctcacc cgggcccccg cccccgcga gcccccggg cgcgcgcgc agcccccg 2400
179   caccgcgac ctcgcctac ggcggcctgc ccgcgcgc ccttgetggg ccgcctgc 2460
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181   acggcgcccc cggccccg gcctccacac gccggccag cagctccaca ccgcgttg 2580
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183   ccggcgccgc cggcggcctg gacccccagg actccgcgc ctgcgcctc tcgtccaa 2700
184   tgtgacctc gccgaccgc ccgcgggccc aggcgggccc ggggcggggc cgtcatccag 2760
185   accaaagcca tgccattgc ctgccccggc gccagtcgc ccagaagcc atagacgaga 2820
186   cgtaggtagc cgtagttgga cggacgggca gggcgggcg ggcagcccc tccgcgccc 2880
187   cggccgtccc cctcatcgc ccgcgcgcca ccccatcgc cctgcccc ggcgcgggc 2940
188   tcgctgca gggggtccc ttcaactcgg tgctcagtt ccccgagctg taagacagg 3000
189   acggggcggc ccagtggctg agaggagccg gctgtggagc ccgcggccc cccaccctc 3060
190   taggtggccc ccgtccgagg aggatcgtt tctaagtga atacttgcc cgcggcttc 3120
191   ccgtgcccc catcgctc acgcaataac cggccggcc ccgtccgc cgcgtcccc 3180
192   ggtgacctc gggagcagca cccgcctcc ctccagcact ggcaccgaga ggcaggcctg 3240
193   gctgcgcagg gcgcggggg gaggtgggg tccgcgcgc gtgatgaatg tactgacgag 3300
194   ccgaggcagc agtgccccca ccgtggcccc ccacgcccc ttaaccccc caccgccatt 3360
195   ccgcgaata aa 3372
197 <210> SEQ ID NO: 3

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198 <211> LENGTH: 1203
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens
201 <400> SEQUENCE: 3
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205         20             25             30
206     Glu Glu Glu Gly Ala Gly Gly Arg Gln Asp Pro Ser Arg Arg Ser Ile
207         35             40             45
208     Arg Leu Arg Pro Leu Pro Ser Pro Ser Pro Ser Ala Ala Ala Gly Gly
209         50             55             60
210     Thr Glu Ser Arg Ser Ser Ala Leu Gly Ala Ala Asp Ser Glu Gly Pro
211         65             70             75             80
212     Ala Arg Gly Ala Gly Lys Ser Ser Thr Asn Gly Asp Cys Arg Arg Phe
213         85             90             95
214     Arg Gly Ser Leu Ala Ser Leu Gly Ser Arg Gly Gly Gly Ser Gly Gly
215         100            105            110
216     Thr Gly Ser Gly Ser Ser His Gly His Leu His Asp Ser Ala Glu Glu
217         115            120            125
218     Arg Arg Leu Ile Ala Glu Gly Asp Ala Ser Pro Gly Glu Asp Arg Thr
219         130            135            140
220     Pro Pro Gly Leu Ala Ala Glu Pro Glu Arg Pro Gly Ala Ser Ala Gln
221         145            150            155            160
222     Pro Ala Ala Ser Pro Pro Pro Pro Gln Gln Pro Pro Gln Pro Ala Ser
223         165            170            175
224     Ala Ser Cys Glu Gln Pro Ser Val Asp Thr Ala Ile Lys Val Glu Gly
225         180            185            190
226     Gly Ala Ala Ala Gly Asp Gln Ile Leu Pro Glu Ala Glu Val Arg Leu
227         195            200            205
228     Gly Gln Ala Gly Phe Met Gln Arg Gln Phe Gly Ala Met Leu Gln Pro
229         210            215            220
230     Gly Val Asn Lys Phe Ser Leu Arg Met Phe Gly Ser Gln Lys Ala Val
231         225            230            235            240
232     Glu Arg Glu Gln Glu Arg Val Lys Ser Ala Gly Phe Trp Ile Ile His
233         245            250            255
234     Pro Tyr Ser Asp Phe Arg Phe Tyr Trp Asp Leu Thr Met Leu Leu Leu
235         260            265            270
236     Met Val Gly Asn Leu Ile Ile Ile Pro Val Gly Ile Thr Phe Phe Lys
237         275            280            285
238     Asp Glu Asn Thr Thr Pro Trp Ile Val Phe Asn Val Val Ser Asp Thr
239         290            295            300
240     Phe Phe Leu Ile Asp Leu Val Leu Asn Phe Arg Thr Gly Ile Val Val
241         305            310            315            320
242     Glu Asp Asn Thr Glu Ile Ile Leu Asp Pro Gln Arg Ile Lys Met Lys
243         325            330            335
244     Tyr Leu Lys Ser Trp Phe Met Val Asp Phe Ile Ser Ser Ile Pro Val
245         340            345            350
246     Asp Tyr Ile Phe Leu Ile Val Glu Thr Arg Ile Asp Ser Glu Val Tyr

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/067,457

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